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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/826,212A

DATE: 04/02/2003

TIME: 13:22:30

14

Input Set : A:\1488.1280006 Seq Lstg.txt
Output Set: N:\CRF4\04022003\I826212A.raw

5 <110> APPLICANT: Wei, Ying-Fei
 7 Yu, Guo-Liang
 9 Gentz, Reiner
 11 Ruben, Steven
 15 <120> TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
 19 <130> FILE REFERENCE: 1488.1280006
 21 <140> CURRENT APPLICATION NUMBER: 09/826,212A
 22 <141> CURRENT FILING DATE: 2001-04-05
 24 <150> PRIOR APPLICATION NUMBER: 09/006,353
 25 <151> PRIOR FILING DATE: 1998-01-13
 27 <150> PRIOR APPLICATION NUMBER: 60/054,885
 28 <151> PRIOR FILING DATE: 1997-08-07
 30 <150> PRIOR APPLICATION NUMBER: 60/035,496
 31 <151> PRIOR FILING DATE: 1997-01-14
 34 <160> NUMBER OF SEQ ID NOS: 26
 38 <170> SOFTWARE: PatentIn version 3.0
 42 <210> SEQ ID NO: 1
 44 <211> LENGTH: 1392
 46 <212> TYPE: DNA
 48 <213> ORGANISM: Homo sapiens
 52 <220> FEATURE:
 54 <221> NAME/KEY: CDS
 56 <222> LOCATION: (183)..(959)
 60 <220> FEATURE:
 62 <221> NAME/KEY: mat_peptide
 64 <222> LOCATION: (261)..()
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 72 <222> LOCATION: (183)..(260)
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 79 agatgcaagg ggtgaaggag cgcttcctac cgttaggaa ctctggggac agagcgcccc 120
 81 ggcgcctga tggccgaggc agggtgcac ccaggaccac ggacggcgtc gggaaaccata 180
 83 cc atg gcc cgg atc ccc aag acc cta aag ttc gtc gtc atc gtc 227
 84 Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val
 85 -25 -20 -15
 87 gcg gtc ctg ctg cca gtc cta gct tac tct gcc acc act gcc cggtc cag 275
 88 Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln
 89 -10 -5 -1 1 5
 91 gag gaa gtt ccc cag cag aca gtg gcc cca cag caa cag agg cac agc 323
 92 Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser
 93 10 15 20
 95 ttc aag ggg gag gag tgt cca gca gga tct cat aga tca gaa cat act 371

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|-----|-------------|------------|------------|--------|------------|------------|------------|------------|--------|--------|--------|------|------|------|------|------|------|
| 96 | Phe | Lys | Gly | Glu | Glu | Cys | Pro | Ala | Gly | Ser | His | Arg | Ser | Glu | His | Thr | |
| 97 | 25 | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | 35 | | |
| 99 | gga | gcc | tgt | aac | ccg | tgc | aca | gag | ggt | gtg | gat | tac | acc | aac | gct | tcc | 419 |
| 100 | Gly | Ala | Cys | Asn | Pro | Cys | Thr | Glu | Gly | Val | Asp | Tyr | Thr | Asn | Ala | Ser | |
| 101 | 40 | | | | | | | | | | | | | | | 50 | |
| 103 | aac | aat | gaa | cct | tct | tgc | ttc | cca | tgt | aca | gtt | tgt | aaa | tca | gat | caa | 467 |
| 104 | Asn | Asn | Glu | Pro | Ser | Cys | Phe | Pro | Cys | Thr | Val | Cys | Lys | Ser | Asp | Gln | |
| 105 | 55 | | | | | | | | | | | | | | | 65 | |
| 107 | aaa | cat | aaa | agt | tcc | tgc | acc | atg | acc | aga | gac | aca | gtg | tgt | cag | tgt | 515 |
| 108 | Lys | His | Lys | Ser | Ser | Cys | Thr | Met | Thr | Arg | Asp | Thr | Val | Cys | Gln | Cys | |
| 109 | 70 | | | | | | | | | | | | | | | 85 | |
| 111 | aaa | gaa | ggc | acc | ttc | cg | aat | gaa | aac | tcc | cca | gag | atg | tgc | cg | aag | 563 |
| 112 | Lys | Glu | Gly | Thr | Phe | Arg | Asn | Glu | Asn | Ser | Pro | Glu | Met | Cys | Arg | Lys | |
| 113 | | | | | | | | | | | | | | | | 100 | |
| 115 | tgt | agt | agg | tgc | cct | agt | ggg | gaa | gtc | caa | gtc | agt | aat | tgt | acg | tcc | 611 |
| 116 | Cys | Ser | Arg | Cys | Pro | Ser | Gly | Glu | Val | Gln | Val | Ser | Asn | Cys | Thr | Ser | |
| 117 | | | | | | | | | | | | | | | | 115 | |
| 119 | tgg | gat | gat | atc | cag | tgt | gtt | gaa | gaa | ttt | ggt | gcc | aat | gcc | act | gtg | 659 |
| 120 | Trp | Asp | Asp | Ile | Gln | Cys | Val | Glu | Glu | Phe | Gly | Ala | Asn | Ala | Thr | Val | |
| 121 | 120 | | | | | | | | | | | | | | | 130 | |
| 123 | gaa | acc | cca | gct | gct | gaa | gag | aca | atg | aac | acc | agc | ccg | ggg | act | cct | 707 |
| 124 | Glu | Thr | Pro | Ala | Ala | Glu | Glu | Thr | Met | Asn | Thr | Ser | Pro | Gly | Thr | Pro | |
| 125 | 135 | | | | | | | | | | | | | | | 145 | |
| 127 | gcc | cca | gct | gct | gaa | gag | aca | atg | aac | acc | agc | cca | ggg | act | cct | gcc | 755 |
| 128 | Ala | Pro | Ala | Ala | Glu | Glu | Thr | Met | Asn | Thr | Ser | Pro | Gly | Thr | Pro | Ala | |
| 129 | 150 | | | | | | | | | | | | | | | 165 | |
| 131 | cca | gct | gct | gaa | gag | aca | atg | acc | acc | agc | ccg | ggg | act | cct | gcc | cca | 803 |
| 132 | Pro | Ala | Ala | Glu | Glu | Thr | Met | Thr | Thr | Ser | Pro | Gly | Thr | Pro | Ala | Pro | |
| 133 | | | | | | | | | | | | | | | | 180 | |
| 135 | gct | gct | gaa | gag | aca | atg | acc | acc | agc | ccg | ggg | act | cct | gcc | cca | gct | 851 |
| 136 | Ala | Ala | Glu | Glu | Thr | Met | Thr | Thr | Ser | Pro | Gly | Thr | Pro | Ala | Pro | Ala | |
| 137 | 185 | | | | | | | | | | | | | | | 195 | |
| 139 | gct | gaa | gag | aca | atg | acc | acc | agc | ccg | ggg | act | cct | gcc | tct | tct | cat | 899 |
| 140 | Ala | Glu | Glu | Thr | Met | Thr | Thr | Ser | Pro | Gly | Thr | Pro | Ala | Ser | Ser | His | |
| 141 | 200 | | | | | | | | | | | | | | | 210 | |
| 143 | tac | ctc | tca | tgc | acc | atc | gta | ggg | atc | ata | gtt | cta | att | gtg | ctt | ctg | 947 |
| 144 | Tyr | Leu | Ser | Cys | Thr | Ile | Val | Gly | Ile | Ile | Val | Leu | Ile | Val | Leu | Leu | |
| 145 | 215 | | | | | | | | | | | | | | | 225 | |
| 147 | att | gtg | ttt | gtt | tgaaagactt | cactgtggaa | gaaattcctt | ccttacctga | | | | | | | | | 999 |
| 148 | Ile | Val | Phe | Val | | | | | | | | | | | | | |
| 149 | 230 | | | | | | | | | | | | | | | | |
| 151 | aaggttcagg | taggcgctgg | ctgaggcg | ggggcg | ggggcg | ctgg | acactctc | gttgc | ccctgc | ccctcc | | | | | | | 1059 |
| 153 | ctctgctgt | ttcccacaga | cagaaacg | cc | tgc | cc | cca | atgc | cc | cc | | | | | | | 1119 |
| 155 | cctggctcta | tcttcctc | tgtgatcg | tc | ccatcccc | atcccgt | cc | ccccc | cc | ccccc | | | | | | | 1179 |
| 157 | ccctggctc | atcgtcc | ctcctgg | gg | ttgggt | cc | ccatct | cc | ccatct | cc | ccatct | | | | | | 1239 |
| 159 | aagaggcagg | gccagttc | cccatcttca | ggccc | ccg | ggcc | ggcc | ggcc | ggcc | ggcc | ggcc | ggcc | ggcc | ggcc | ggcc | ggcc | 1299 |
| 161 | tcaactgggt | gacaagggt | aggatg | gaa | gtgt | tcacgg | gat | tttatt | ca | gc | tttgg | tc | | | | | 1359 |
| 163 | gaggcagaaca | caga | gat | ttt | ccgt | gaaaaaaa | aaa | | | | | | | | | | 1392 |

166 <210> SEQ ID NO: 2

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Input Set : A:\1488.1280006 Seq Lstg.txt
Output Set: N:\CRF4\04022003\I826212A.raw

168 <211> LENGTH: 259
170 <212> TYPE: PRT
172 <213> ORGANISM: Homo sapiens
176 <400> SEQUENCE: 2
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182 Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu
183 -10 -5 -1 1 5
186 Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe
187 10 15 20
190 Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly
191 25 30 35
194 Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
195 40 45 50
198 Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys
199 55 60 65 70
202 His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln Cys Lys
203 75 80 85
206 Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys Arg Lys Cys
207 90 95 100
210 Ser Arg Cys Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp
211 105 110 115
214 Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala Thr Val Glu
215 120 125 130
218 Thr Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala
219 135 140 145 150
222 Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro
223 155 160 165
226 Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala
227 170 175 180
230 Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala
231 185 190 195
234 Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr
235 200 205 210
238 Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Leu Ile
239 215 220 225 230
242 Val Phe Val
246 <210> SEQ ID NO: 3
248 <211> LENGTH: 455
250 <212> TYPE: PRT
252 <213> ORGANISM: Homo sapiens
256 <400> SEQUENCE: 3
258 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Pro Leu Val Leu Leu
259 1 5 10 15
261 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
262 20 25 30
264 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
265 35 40 45
267 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys

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| 268 | 50 | 55 | 60 | | | | | | | | | | | | | |
| 270 | Gly | Thr | Tyr | Leu | Tyr | Asn | Asp | Cys | Pro | Gly | Pro | Gly | Gln | Asp | Thr | Asp |
| 271 | 65 | | | | | | | | | | | | | | | 80 |
| 273 | Cys | Arg | Glu | Cys | Glu | Ser | Gly | Ser | Phe | Thr | Ala | Ser | Glu | Asn | His | Leu |
| 274 | | | | | | | | | | | | | | | 95 | |
| 276 | Arg | His | Cys | Leu | Ser | Cys | Ser | Lys | Cys | Arg | Lys | Glu | Met | Gly | Gln | Val |
| 277 | | | | | | | | | | | | | | | 110 | |
| 279 | Glu | Ile | Ser | Ser | Cys | Thr | Val | Asp | Arg | Asp | Thr | Val | Cys | Gly | Cys | Arg |
| 280 | | | | | | | | | | | | | | | 125 | |
| 282 | Lys | Asn | Gln | Tyr | Arg | His | Tyr | Trp | Ser | Glu | Asn | Leu | Phe | Gln | Cys | Phe |
| 283 | | | | | | | | | | | | | | | 140 | |
| 285 | Asn | Cys | Ser | Leu | Cys | Leu | Asn | Gly | Thr | Val | His | Leu | Ser | Cys | Gln | Glu |
| 286 | 145 | | | | | | | | | | | | | | 160 | |
| 288 | Lys | Gln | Asn | Thr | Val | Cys | Thr | Cys | His | Ala | Gly | Phe | Phe | Leu | Arg | Glu |
| 289 | | | | | | | | | | | | | | | 175 | |
| 291 | Asn | Glu | Cys | Val | Ser | Cys | Ser | Asn | Cys | Lys | Lys | Ser | Leu | Glu | Cys | Thr |
| 292 | | | | | | | | | | | | | | | 190 | |
| 294 | Lys | Leu | Cys | Leu | Pro | Gln | Ile | Glu | Asn | Val | Lys | Gly | Thr | Glu | Asp | Ser |
| 295 | | | | | | | | | | | | | | | 205 | |
| 297 | Gly | Thr | Thr | Val | Leu | Leu | Pro | Leu | Val | Ile | Phe | Phe | Gly | Leu | Cys | Leu |
| 298 | | | | | | | | | | | | | | | 220 | |
| 300 | Leu | Ser | Leu | Leu | Phe | Ile | Gly | Leu | Met | Tyr | Arg | Tyr | Gln | Arg | Trp | Lys |
| 301 | 225 | | | | | | | | | | | | | | 240 | |
| 303 | Ser | Lys | Leu | Tyr | Ser | Ile | Val | Cys | Gly | Lys | Ser | Thr | Pro | Glu | Lys | Glu |
| 304 | | | | | | | | | | | | | | | 255 | |
| 306 | Gly | Glu | Leu | Glu | Gly | Thr | Thr | Lys | Pro | Leu | Ala | Pro | Asn | Pro | Ser | |
| 307 | | | | | | | | | | | | | | | 270 | |
| 309 | Phe | Ser | Pro | Thr | Pro | Gly | Phe | Thr | Pro | Thr | Leu | Gly | Phe | Ser | Pro | Val |
| 310 | | | | | | | | | | | | | | | 285 | |
| 312 | Pro | Ser | Ser | Thr | Phe | Thr | Ser | Ser | Ser | Thr | Tyr | Thr | Pro | Gly | Asp | Cys |
| 313 | | | | | | | | | | | | | | | 300 | |
| 315 | Pro | Asn | Phe | Ala | Ala | Pro | Arg | Arg | Glu | Val | Ala | Pro | Pro | Tyr | Gln | Gly |
| 316 | 305 | | | | | | | | | | | | | | 320 | |
| 318 | Ala | Asp | Pro | Ile | Leu | Ala | Thr | Ala | Leu | Ala | Ser | Asp | Pro | Ile | Pro | Asn |
| 319 | | | | | | | | | | | | | | | 335 | |
| 321 | Pro | Leu | Gln | Lys | Trp | Glu | Asp | Ser | Ala | His | Lys | Pro | Gln | Ser | Leu | Asp |
| 322 | | | | | | | | | | | | | | | 350 | |
| 324 | Thr | Asp | Asp | Pro | Ala | Thr | Leu | Tyr | Ala | Val | Val | Glu | Asn | Val | Pro | Pro |
| 325 | | | | | | | | | | | | | | | 365 | |
| 327 | Leu | Arg | Trp | Lys | Glu | Phe | Val | Arg | Arg | Leu | Gly | Leu | Ser | Asp | His | Glu |
| 328 | | | | | | | | | | | | | | | 380 | |
| 330 | Ile | Asp | Arg | Leu | Glu | Leu | Gln | Asn | Gly | Arg | Cys | Leu | Arg | Glu | Ala | Gln |
| 331 | 385 | | | | | | | | | | | | | | 400 | |
| 333 | Tyr | Ser | Met | Leu | Ala | Thr | Trp | Arg | Arg | Arg | Thr | Pro | Arg | Arg | Glu | Ala |
| 334 | | | | | | | | | | | | | | | 415 | |
| 336 | Thr | Leu | Glu | Leu | Leu | Gly | Arg | Val | Leu | Arg | Asp | Met | Asp | Leu | Leu | Gly |
| 337 | | | | | | | | | | | | | | | 430 | |
| 339 | Cys | Leu | Glu | Asp | Ile | Glu | Glu | Ala | Leu | Cys | Gly | Pro | Ala | Ala | Leu | Pro |
| 340 | | | | | | | | | | | | | | | 445 | |
| | 435 | | | | | | | | | | | | | | | |

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Input Set : A:\1488.1280006 Seq Lstg.txt
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343 450 455
345 <210> SEQ ID NO: 4
347 <211> LENGTH: 461
349 <212> TYPE: PRT
351 <213> ORGANISM: Homo sapiens
355 <400> SEQUENCE: 4
357 Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
358 1 5 10 15
360 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
361 20 25 30
363 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
364 35 40 45
366 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
367 50 55 60
369 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
370 65 70 75 80
372 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
373 85 90 95
375 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
376 100 105 110
378 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
379 115 120 125
381 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
382 130 135 140
384 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
385 145 150 155 160
387 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
388 165 170 175
390 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
391 180 185 190
393 Asn Ala Ser Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
394 195 200 205
396 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
397 210 215 220
399 Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
400 225 230 235 240
402 Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
403 245 250 255
405 Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
406 260 265 270
408 Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
409 275 280 285
411 Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
412 290 295 300
414 Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
415 305 310 315 320
417 Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
418 325 330 335

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 04/02/2003
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Input Set : A:\1488.1280006 Seq Lstg.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:15; N Pos. 425,434,438,446,458,474,478,487,489,496,499,503

Seq#:16; N Pos. 41,301,302,314,317,326

Seq#:17; N Pos. 54,55,59,62,72,134,172,181,235,269,282,308,309,338

Seq#:18; N Pos. 13,34,78,82,84,197,204,218,220,226